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PRINCIPAL INVESTIGATOR: Hua Zhao, Ph.D.

CONTRACTING ORGANIZATION: Health Research, Inc.  
Buffalo, NY 14263

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14. ABSTRACT In the past one year, we have successfully obtained the DNA samples and epidemiologic questionnaire data as well as setting up the genotyping assays. So far, we have DNA samples from 1200 cases (600 CAs and 600 AAs) and 1200 healthy controls (600 CAs and 600 AAs). The first batch of genotyping is in the process.					
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## Table of Contents

	<u>Page</u>
Introduction.....	4
Body.....	4
Key Research Accomplishments.....	4
Reportable Outcomes.....	4
Conclusion.....	5

## INTRODUCTION

In current proposal, we propose to conduct a molecular-based case-control study to evaluate the genetic polymorphisms in selected miRNA genes, responsive elements in target genes, and miRNA processing genes as predictors of breast cancer risk. The study population will consist of 1000 breast cancer patients and 1000 healthy controls. We will also plan to screen germ-line mutations in selected miRNA genes in 120 AA breast cancer patients who are diagnosed at early age and have aggressive diseases with poor prognosis. The proposed research will utilize biological specimens and epidemiological data from breast cancer patients and healthy controls systematically collected by an existing study. We will integrate epidemiologic and clinical data with the genetic data from the studies. In further exploratory analysis, we will evaluate whether SNPs in miRNA genes that are predicted to regulate key breast cancer genes, SNPs in responsive elements in these key genes, and haplotypes in miRNA processing genes (*Drosha*, *Dicer*, *DGCR8*, *XPO5*, *TRBP* and *AGO2*) are associated with early age at diagnosis and aggressive disease characteristics (high-grade tumors and ER-negative status) in AA women.

## BODY

In the past one year, we have successfully obtained the DNA samples and epidemiologic questionnaire data as well as setting up the genotyping assays. So far, we have DNA samples from 1200 cases (600 CAs and 600 AAs) and 1200 healthy controls (600 CAs and 600 AAs). The first batch of genotyping is in the process. This batch will include 124 SNPs proposed in the study, namely 57 SNPs in miRNA genes and 67 tagSNPs in miRNA processing genes. The pre-tests for all the SNP analyses have been completed.

## KEY RESEARCH ACCOMPLISHMENTS

We have successfully obtained the DNA samples and epidemiologic questionnaire data as well as setting up the genotyping assays. So far, we have DNA samples from 1200 cases (600 CAs and 600 AAs) and 1200 healthy controls (600 CAs and 600 AAs).

124 SNPs proposed in the study, namely 57 SNPs in miRNA genes and 67 tagSNPs in miRNA processing genes, are in the process of genotyping. The pre-tests for all the SNP analyses have been completed.

## REPORT OUTCOME

Due to the nature of the study, we haven't produced the data yet. No significant outcomes are reported at this time.

## **CONCLUSIONS**

So far, the study moves smoothly. We don't expect any problems at current stage. We expect to have ample data to report in second year.